

## **SEQUENCE LISTING**

**SEQ ID NO: 1 - SARS Coronavirus Urbani S-protein full-length gene sequence (AY278741, 3768 bps)**

aagaattgaccgcctcaatgaggtcgctaaaattaaatgaatcactcattgaccccaagaattggaaaatatgag  
caatatataatggcccttggatgtttggctcgcccttcattgctggactaattgcacatgtcatggttacaatctgttttt  
gcatgacttagttgtgcagtgcctcaagggtgcattgtgggtttgtcaagttgtgaggatgactctgagcc  
agttctcaagggtgtcaaattacattacacataa

**SEQ ID NO: 2 - Protein sequence for full length S-protein from accession number AAP13441 corresponding to the gene AY278741 (1256aa)**

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRS  
DTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRG  
WVFGSTMNNKSQSVIINNSTNVIRACNFELCDNPFFAVSKPMGTQTHM  
IFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKGFLYVYKGYQPI  
DVVRDLPNGFNTLKPIFKLPLGINITNFRAILTAFSPAQDWGTSAAA YFVG  
YLKPTTFMLKYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFR  
VVPSGDVVRFPNITNLCPGEVFNAVKFPSVYAWERKKISNCVADYSVLY  
NSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIA  
DNYKLPDDFMGCVLAWNTRNIDATSTGNYNKYRYLHGKLRPFERDI  
SNVPFSPDGKPCTPPALNCYWPLNDYGFYTTGIGYQPYRVVVLSEELLNA  
PATVCGPLKLSTDLIKNQCVNFNGLTGTGVLTPSSKRFQPFQQFGRDVSD  
FTDSVRDPKTSEILDISPCSF GGVSITPGTNASSEAVLYQDVNCTDVSTA  
IHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYH  
TVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMA  
KTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVF  
AQVKQMYKPTLK YFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGF  
MKQYGECLGDINARDLICAQKFNGLTVPPLLTDDMIAAYTAALVSGTAT  
AGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVL YENQKQIANQFNKAIS  
QIQESLT TSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLDILSRL  
DKVEAEVQIDRLITGRLQLSQLTYVTQQLIRAAEIRASANLAATKMSECVLG  
QSKRVDFCGKGYHLMSPFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG  
KAYFPREGVFVFNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVY  
DPLQPELDSFKEELDKYFKNHTSPDVLDGDISGINASVVNIQKEIDRLNEVA  
KNLNESLIDLQELGKYEQYIKWPWVWLGFIAGLIAIVMVTILLCCMTSCC  
SCLKGACSCGSCCKFDEDDEPVLKGVLHYT

**SEQ ID NO: 3 - Protein sequence for Spike protein amino acid 275-1081 from accession number AAP13441 (807aa) (wild type, wt):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPAGDVVRFPNITNLC  
PFGEVFNAFKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK  
LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADNYKLPPDFMGCVLA  
WNTRNIDATSTGNYNKYRYLHGKLRPFERDISNVPFSPDGKPCTPPALN  
CYWPLNDYGFYTTGIGYQPYRVVVLSEELLNAPATVCGPKLSTDLIKQNQ  
CVNFNFNGLTGTGVLTTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISP  
CSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN  
NVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYT  
MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE  
CANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG  
GFNFSQILPDPLKPTKRSFIEDLLFNKVTADAGFMKQYGECLGDINARDLI  
CAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM  
QMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQUESTTSTALGKLQDV  
VNQNAQALNTLVKQLSSNFGAISSVLDILSRLDKVEAEVQIDRLITGRLQS  
LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDLFCGKGYHLMSFP  
QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVFVFNG

**SEQ ID NO: 4 - Protein sequence for Spike protein amino acid 275-1081 mutant with 9 potential N-linked glycosylation sites eliminated (807aa)(substituted Alanine shown as "a") (mutant, mt):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNlaNLCP  
FGEVFaATKFPSVYAWERKKISNCADYSVLYNSeAFFSTFKCYGVSATKLN  
DLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNKLPDDFMGCVLAWN  
TRNIDATSTGNYYKYRYLRHGKLRFERDISNVPSPDGKPCTPPALNCY  
WPLNDYGFYTTGIGYQPYRVVVLNFELLNAPATVCGPLSTDLIKNCV  
NFNFNGLTGTGVLTTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCS  
FGGVSVITPGTNAaSEVAVLYQDVaCTDVSTAIHADQLTPAWRIYSTGNNV  
FQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMS  
LGADSSIAYSaNTIAIPTNFaISITTEVMPVSMAKTSVDCNMYICGDSTECAN  
LLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFN  
FaQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ  
KFNGLTVLPLLTDDMIAAYTAALVSGTATAGWTFGAGAAALQIPFAMQM  
AYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTSTALGKLQDVVN  
QNAQALNTLVKQLSSNFGAISSVLDILSRDKVEAEVQIDRLITGRLQSLQ  
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQA  
APHGVVFLHVTYVPSQERNFaTAPAICHEGKA YFPREGVFVFNG

**SEQ ID NO: 5** - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with native virus codons and elimination of N-glycosylation sites (2421bp) (substituted nucleotides shown capitalized):

gctgttgtttctcaaaaatccacttgctgaactcaaatacgctgttaagagcttgagattgacaaaggaaatttacc  
agacctctaattcagggttgcctcaggagatgtgtgagattccataattGcaaacttgctgccttggagaggtt  
tttGCCgctactaaattccctctgtcatgcatggagaaaaaaaattctaattgtgtgctgattactctgtctaca  
caactcaGcatttttcaccccttaagtgcatacgccgttgcctcactaagttgaatgatcttgcctcataatgtctatgca  
gattttttgttagtcaagggagatgatgtaagacaaaatagcgccaggacaaactggttattgctgattataattataat  
tgccagatgattcatgggtgtcctgcttggaaatacttaggaacattgatgacttcaactggttaattataattataat  
ataggatcttagacatggcaagcttgcggccattttgagagagacatacttaatgtgccttccctgtggcaaaacctt  
gcacccccacccctgtcttaattgttattggcattaaatgattatggttttacaccactactggcattggctaccaaccc  
gagttgttagtactttttaactttaatgcacccggccacgggtgtgaccaaaattatccactgaccattataagaac  
cagtgtgtcaatttaatttaatggactcactgtactgggtgttaactccctctcaaaagagatttcaaccattcaacaat  
ttggccgtgtttctgatttcactgattccgttgcagatcttcaatttacatctgaaatattagacattcacccctgtctttgg  
gggtgttagttagttaatttacacccctggaaacaatgtGcatctgaagtgtgttctatataatcaagatgttGCctgcactgt  
tttctacagcaattcatgcagatcaactcacccagctggcgcatataatttacttggaaacaatgttacccagactcaag  
caggctgtttataggagactgagcatgtcgacacttctttagtgcacattccattggagctggcattttgtctgtt  
ccatacagtttttattacgttagtactagccaaaaatctattgtggcttatactatgtctttagtgcgtatgttcaattgtt  
actctGCCaaccaccattgtctatactacttGcaatttagcattactacagaagtaatgcctgttctatggctaaaa  
cctccgttagattgtaatatgtacatctgcggagattctactgaatgtgctaaatttgcttccaaatatggtagctttgcacac  
aactaaatgtgcactctcaggattgtctgaacaggatgcacacacacgtgaagtgtcgctcaagtcaacaaaat  
gtacaaaaccccaactttgaaatattttgggttttaatttGcacaaatattacctgaccctctaaagccaactaagagg  
tcttttattttaggacttgccttaataaggtgacactcgctgtgctggctcatgaagcaatatggcgaatgccttaggt  
atattaatgttagagatctatttgcgccagaagtcaatggacttacagttgtgcacccatctgtctactgtatgtt  
gctgcctacactgtcttagttgttagtggacttgcactgtggatggacattttgggtctggcgtcttcaaaatacc  
ttgtctatgcaatggcatataggtaatggcattggagttacccaaaatgttctatgagaacccaaaacaaaatgc  
accatattacaaggcgatttagtcaaattcaagaatcactacaacaactcaactgcattggcaagctgcaagacgtt  
gttaaccagaatgctcaagcattaaacacacttgttaaacaacttagcttaattttgggtcaattcaagtgtctaaat  
tatccittcgcacttgataaaagtgcggagggtacaatttgacaggtaattacaggcagacttcaaaaggccctcaaa  
cctatgttaacacaacaactaatcaggcgtctgaaatcaggcgtctgtaatctgtctactaaaatgtctgatgt  
tctggacaataaaaagagttgactttgtggaaaggcgtaccacccatgtccttcccacaagcagccccgtatgt  
ttgtcttctacatgtcactgtgtggccatcccaggagaggaacttcGccacagcgcagcaattgtcatgaaggcaa  
agcatactccctcgtaagggttttgcattttatggc

**SEQ ID NO: 6 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with altered codon usage to enhance expression and elimination of N-glycosylation sites (2421bp):**

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GCCGTGGACTGCTCCCAGAACCCCTGGCCGAGCTGAAGTGCTCCGTGAAGT
CCTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTGGTGCCTC
CGGCGACGTGGTGCCTCCCCAACATGCCAACCTGTGCCCCCTCGGGAGGTG
TTCGCCGCCACCAAGTTCCCCTCCGTGTACGCCCTGGGAGCGAAGAAGATCTCCA
ACTGCGTGGCCGACTACTCCGTGCTGTACAACCTCCGCCCTCTTCTCCACCTCAA
GTGCTACGGCGTGTCCGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTAC
GCCGACTCCTCGTGGTGAAGGGCGACGACGTGCCAGATGCCCGGCCAGA
CGGGCGTGTACGCCGACTACAACCTACAAGCTGCCGACGACTTCATGGCTGCGT
GCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGAACTACAACCTAC
AAGTACCGCTACCTGCGCCACGGCAAGCTGCCCGACTTCGAGCGCGACATCTCCA
ACGTGCCCTCTCCCCCGACGGCAAGCCCTGCACCCCCCGGCCCTGAACGTGCTA
CTGGCCCTGAACGACTACGGCTTCTACACCACCACGGCATCGCTTACAGCCC
TACCGCGTGGTGGTGTCTGCTTCAGCTGCTGAACGCCCGCCACCGTGTGCG
GCCCGAAGCTGTCCACCGACCTGATCAAGAACCAAGTGCCTGAACATTCAA
CGGCCTGACCGGCACCGCGTGTGACCCCCCTCCAAAGCGCTTCCAGGCCCTTC
CAGCAGTTGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCCGACCCAAAGA
CCTCCGAGATCCTGGACATCTCCCCCTGCTCTCGGGCGTGTCCGTGATCAC
CCCCGGCACCAACGCCCTCCGAGGTGGCCGTGTACCAAGGACGTGGCCTGC
ACCGACGTGTCCACCGCCATCCACGCCGACCGAGCTGACCCCCCGCTGGCGCATCT
ACTCCACCGGCAACAAACGTGTTCCAGACCCAGGGCGCTGCCTGATGGCGCCGA
GCACGTGGACACCTCCTACGAGTGCACATCCCCATGGCGCCGGCATGCGCC
TCCTACCACACCGTGTCCCTGCTGCCCTCACCTCCAGAAGTCCATCGTGGCCT
ACACCATGTCCTGGCGCCGACTCCTCCATCGCCTACTCCGACAAACACCATCGC
CATCCCCACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCGTGTCATG
GCCAAGACCTCCGTGGACTGCAACATGTACATCTGCCGACTCCACCGAGTGCG
CCAACCTGCTGCTGAGTACGGCTCTGCAACCGAGCTGAACCGGCCCTGTC
CGGCATCGCCGCCGAGCAGGACCGCAACACCCCGAGGTGTTGCCCGAGGTGAAG
CAGATGTACAAGACCCCCACCCCTGAAGTACTCGGCGGCTTCAACTCGCCAGA
TCCTGCCCGACCCCCCTGAAGCCCACCAAGCGCTCTTCATCGAGGACCTGCTGTT
CAACAAGGTGACCCCTGGCCGACGCCGCTTCATGAAGCAGTACGGCGAGTGCTG
GGCGACATCAACGCCCGCAGCTGATCTGCCCTCACCGCCGCCCTGACCG
TGCTGCCCGACCGACGACATGATGCCGCCTACACCGCCGCCCTGGT
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCCTGCAGATC
CCCTCGCCATGCAGATGGCCTACCGCTTCAACGGCATGGCGTACCCAGAACG
TGCTGTACGAGAACAGAGCAGATGCCAACCAAGTCAACAAGGCCATCTCCCA
GATCCAGGAGTCCCTGACCAACCTCCACCGCCCTGGGCAAGCTGCAGGACGTG
GTGAACCAGAACGCCAGGGCCCTGAACACCCCTGGTGAAGCAGCTGTCCCTCAA
TCGGCGCCATCTCCCGTGTGAACGACATCTGTCCGCCCTGGACAAGGTGGA
GGCGAGGTGCAGATCGACCGCCTGATCACCGGCCCTGCAGTCCCTGCAGACC
TACGTGACCCAGCAGCTGATCCGCCGCCGAGATCCGCCCTCGCCAAACCTGG
CCGCCACCAAGATGTCCGAGTGCCTGGGCCAGTCCAAGCGCGTGGACTCTG
CGGCAAGGGCTACCACCTGATGTCCCTCCCCCAGGCCCGCCCCCACGGCGTGGT
TTCCCTGCACGTGACCTACGTGCCCTCCCAGGAGCGCAACTCGCCACCGCCCG
CCATCTGCCACGAGGGCAAGGCCTACTTCCCCCGCGAGGGCGTGTGTTCAA
CGGC

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**SEQ ID NO: 7 - Potential N-glycosylation sites within the protein sequence of the Spike protein amino acid 275-1081 (807aa) (wild type, wt) with potential N-glycosylation sites underlined.**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLC  
 PFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK  
 LNLDLCSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA  
 WNTRNIDATSTGN<sup>Y</sup>NYK<sup>Y</sup>RYLRHGKL<sup>R</sup>PFERDISNVPFSPDGKPC<sup>T</sup>PPALN  
 CYWPLNDYGF<sup>TTT</sup>GIGYQPYRVV<sup>V</sup>LSFELLNAPATVC<sup>G</sup>PKL<sup>S</sup>DLIKNQ  
 CVNFNFNGLTGTGVLT<sup>SS</sup>KRFQPFQQFGRDVSDFTDSVRDPKTSEILDISP  
 CSFGGVSVITPGTNAASEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN  
 NVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTV<sup>SLL</sup>RSTSQKSIVAYT  
 MSLGADSSIAYSNNTIAPTNF<sup>S</sup>I<sup>S</sup>ITTEVMPV<sup>M</sup>AKTSVDCNMYICGDSTE  
 CANLLLQYGSFCTQLNR<sup>A</sup>LSGIAAEQDRNTREVFAQVKQMYK<sup>T</sup>PTLK<sup>Y</sup>F<sup>G</sup>  
 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI  
 CAQKFNGLT<sup>V</sup>L<sup>P</sup>PLLTDDMIAAYTAALVSGTATAGWTFGAGAA<sup>L</sup>QIPFAM  
 QMA<sup>Y</sup>RFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTSTALGKLQDV  
 VNQNAQALNTLVQLSSNFGAISSVLNDILSR<sup>L</sup>DKVEAEVQIDRLITGRLQS  
 LQTYVTQQLIRAAEIRASANLAATKMSEC<sup>V</sup>L<sup>G</sup>QSKRVD<sup>F</sup>CGKG<sup>Y</sup>HLM<sup>S</sup>FP  
 QAA<sup>A</sup>PHGVVF<sup>L</sup>HVTYVPSQERNFT<sup>T</sup>APAICHEGKAYFPREGVFVNG

**SEQ ID NO: 8 Amino acid sequence of Region II peptide**

VLYNSAFFSTFKCYGVSATKLNDLCSNVYADSFVVKGDDVRQIAPGQTGVIADY  
 NYKLPDDFMGCVLAWNTRNIDATSTGN<sup>Y</sup>NYK<sup>Y</sup>RYLRHGKL<sup>R</sup>PFERDISNVPFSP  
 DGKPC<sup>T</sup>PPALNCYWPLNDYGF<sup>TTT</sup>GIGYQPYRVV<sup>V</sup>LSFELLNAPATVC<sup>G</sup>PKL<sup>S</sup>  
 DLIKNQCVNFNFNGLTGTGVLT<sup>SS</sup>KRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS  
 PCSFGGVSVITPGTNAASEVAVLYQDV

**SEQ ID NO: 9 Amino acid sequence of Region III peptide**

AEQDRNTREVFAQVKQMYK<sup>T</sup>PTLK<sup>Y</sup>F<sup>G</sup>GFNF<sup>A</sup>QILPDPLKPTKRSFIEDLLFNKV  
 TLADAGFMKQYGECLGDINARDLICAQKFNGLT<sup>V</sup>L<sup>P</sup>PLLTDDMIAAYTAALVSGT  
 ATAGWTFGAGAA<sup>L</sup>QIPFAMQMA<sup>Y</sup>RFNGIGVTQNVLYENQKQIANQFNKAISQIQ  
 ESLTTSTALGKLQDVVNQNAQALNTLVQLSSNFGAISSVLNDILSR<sup>L</sup>DKVEAEV  
 QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSEC<sup>V</sup>L<sup>G</sup>QSKRVD<sup>F</sup>CGKG  
 YHL

**SEQ ID NO: 10 Amino acid sequence of Region IV peptide**

VLYNSAFFSTFKCYGVSATKLNDLCSNVYADSFVVKGDDVRQIAPGQTGVIADY  
 NYKLPDDFMGCVLAWNTRNIDATSTGN<sup>Y</sup>NYK<sup>Y</sup>RYLRHGKL<sup>R</sup>PFERDISNVPFSP  
 DGKPC<sup>T</sup>PPALNCYWPLNDYGF<sup>TTT</sup>GIGYQPYRVV<sup>V</sup>LSFELLNAPATVC<sup>G</sup>PKL<sup>S</sup>  
 DLIKNQCVNFNFNGLTGTGVLT<sup>SS</sup>KRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS  
 PCSFGGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQLTPAWRIYSTGN<sup>NN</sup>VF

QTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSS  
IAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCT  
QLNRALSGIAAEQDRNTREVFAQVKQMYKPTPLKYFGGFNFAQILPDPLKPTKRS  
FIEDLLFNKVTLADAGFMKQYGECLGDNARDLICAQKFNGLTVLPPPLTDMMIA  
AYTAALVSGTAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIA  
NQFNKAISQIQESLTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI  
LSRLDKVEAEVQIDRLITGRLQLSQLTYVTQQLIRAAEIRASANLAATKMSECVLGQ  
SKRVDFCGKGYHL

**SEQ ID NO: 11 Amino acid sequence of Region II peptide from Spike protein from accession number AAP13441(wild type)**

VLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQ  
 TGVIAADNYKLPDDFMGCVLAWNTRNIDATSTGNYYKYRYLRHGKL RP  
 FERDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTGIGYQPYRVVVLSF  
 ELLNAPATVCGPKLSTDLIKNQCVNFNGLTGTGVLTPSSKRFQPFQQFG  
 RDVSDFTDSVRDPKTSEILDISPCSFGGVSITPGTNASSEAVLYQDV

**SEQ ID NO: 12 Amino acid sequence of Region III peptide from Spike protein from accession number AAP13441(wild type)**

AEQDRNTREVFAQVKQMYKPTPLKYFGGFNFSQLPDPLKPTKRSFIED  
 LLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVPPLLTDDMI  
 AAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYEN  
 QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNF  
 GAISSVLNDILSRLDKVEAEVQIDRLITGRLQLTYVTQQLIRAAEIRASAN  
 LAATKMSECVLGQSKRVDFCGKGYHL

**SEQ ID NO: 13 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):**

VLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPQTG  
 VIADNYKLPDDFMGCVLAWNTRNIDATSTGNYYKYRYLRHGKL RPFE  
 RDISNVPFSPDGKPCPPALNCYWPLNDYGFYTTGIGYQPYRVVVLSFEL  
 LNAPATVCGPKLSTDLIKNQCVNFNGLTGTGVLTPSSKRFQPFQQFGRD  
 VSDFTDSVRDPKTSEILDISPCSFGGVSITPGTNASSEAVLYQDVNCTDV  
 STAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICA  
 SYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVS  
 MAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTRE  
 VFAQVKQMYKPTPLKYFGGFNFSQLPDPLKPTKRSFIEDLLFNKVTLADA  
 GFMKQYGECLGDINARDLICAQKFNGLTVPPLLTDDMIAAYTAALVSGT  
 ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKA  
 ISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILS  
 RLDKVEAEVQIDRLITGRLQLTYVTQQLIRAAEIRASANLAATKMSECV  
 LGQSKRVDFCGKGYHL

**SEQ ID NO: 14 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSGDVVRFPNITNLCPFG  
EVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATKLND  
LCFSNVYADSFVVKGDDVRQIAPGQTGVIADNYKLPDDFMGCVLAWNT  
RNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCY  
WPLNDYGFYTTGIGYQPYRVVVLSELNAPATVCGPLSTDLIKQNQCV  
NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDSVRDPKTSEILDISPCS  
FGGVSVITPGTNASSEVAVL YQDVNCTDVSTAIHADQLTPAWRIYSTGNN  
VFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTM  
SLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTECA  
NLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGF  
NFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICA  
QKFNGLTVPPLLDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQ  
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTSTALGKLQDVV  
NQNAQALNTLVKQLSSNFGAISSVLNDLSRLDKVEAEVQIDRLITGRLQSL  
QTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL

**SEQ ID NO: 15 Linker for nucleotide primer oligo #1**

TCGCTCGAGAAAAGAGTGCTCTACAACTCAGCATT

**SEQ ID NO: 16 Linker for nucleotide primer oligo #2**

ATCTCTAGATTAAACATCTTGATATAGAACAGC

**SEQ ID NO: 17 Linker for nucleotide primer oligo #3 TCGCTCGAG**

AAAAGAGCTGAACAGGGATCGAACACA

**SEQ ID NO: 18 Linker for nucleotide primer oligo #4**

ATCTCTAGATTAAAGGTGGTAGCCCTTCC

**SEQ ID NO: 19 SARS Spike Glycoprotein Fragment synthetic DNA sequence with N-lined glycosylation site mutations (2421 bp)**

GCCGTGGACTGCTCCCAGAACCCACTGGCCGAGCTGAAGTGCTCCGTGA  
AGTCCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAATTCGCGTG  
GTGCCATCCGGCACGTGGTGCCTCCAAACATGCCAACCTGTGCC

CATTGGCGAGGTGTTGCCGCCACCAAGTCCCATCCGTGTACGCCCTG  
 GGAGCGCAAGAAGATCTCCAACCGTGGCCGACTACTCCGTG  
 CTGTACAACCTCCGCCTCTTCTCCACCTCAAGTGCTACGGCGTGTCCGC  
 CACCAAGCTGAACGACCTGTGCTTCTCAACAGTGTACGCCGACTCCTCG  
 TGGTGAAGGGCGACGACGTGCGCCAGATGCCAGGCCCCAGGCCAGACCGCGT  
 GATGCCGACTACAACCTACAAGCTGCCAGACGACTTCATGGGCTGCGTG  
 CTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACA  
 ACTACAAGTACCGCTACCTGCGCACGGCAAGCTGCCAGGCTTCTGAGCG  
 CGACATCTCCAACGTGCCATTCTCCCAGACGCCAGGCAAGCCATGCCACCCAC  
 CAGCCCTGAACTGCTACTGCCACTGAACGACTACGGCTTCTACACCACC  
 ACCGGCATCGGCTACCCAGCCATACCGCGTGGTGGTGTCTGCTCGAGC  
 TGCTGAACGCCAGCCACCGTGTGCGGCCAAAGCTGTCCACCGACCT  
 GATCAAGAACCAAGTGCCTGAACCTCAACTCAACGCCGACCCGGCACC  
 GGCGTGTGACCCATCTCCAAGCGCTCCAGCCATTCCAGCAGTCGG  
 CCGCGACGTGTCCGACTTCACCGACTCCGTGCCGACCCAAAGACCT  
 CCGAGATCTGGACATCTCCCATGCTCTCGCGGGCGTGTCCGTGATC  
 ACCCCAGGCACCAACGCCCTCCGAGGTGGCCGTGTACCAAGGACG  
 TGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCGACTGACCC  
 AGCCTGGCGCATCTACTCCACCGCAACAAACGTGTTCCAGACCCAGGCC  
 GGCTGCCTGATCGGCGCCGAGCACGTGGACACCTCTACGAGT  
 GCGACATCCAATCGGCGCCGGCATCTGCCCTCCTACCAACACCGTGTG  
 CCTGCTGCGCTCCACCTCCCAGAAGTCCATCGTGGCCTACACCATGTCCC  
 TGGCGCCGACTCCTCCATGCCCTACTCCGCCAACACCATGCCATCCA  
 ACCAACTCGCCATCTCCATCACCACCGAGGTGATGCCAGTGTCCATGGC  
 CAAGACCTCCGTGGACTGCAACATGTACATCTGCCGACTCCACCGAG  
 TGCGCCAACCTGCTGCTGCCAGTACGGCTCCTCTGCACCCAGCTGAACCG  
 CGCCCTGTCCGGCATGCCGCCGAGCAGGACCGAACACCCCGAGGTG  
 TTCGCCAGGTGAAGCAGATGTACAAGACCCCAACCTGAAGTACTTCG  
 GCGGCTTCAACTCGCCCAGATCCTGCCAGACCCACTGAAGCCAACCAA  
 GCGCTCTTCATCGAGGACCTGCTGTTCAACAAAGGTGACCCCTGGCGAC  
 GCCGGCTTCATGAAGCAGTACGGCGAGTGCCTGGCGACATCACGCC  
 GCGACCTGATCTGCCAGAAGTCAACGCCCTGACCGTGTGCCACC  
 ACTGCTGACCGACGACATGATGCCGCCCTACACCGCCGCCCTGGTGTG  
 CGGCACCGCCACCGCCGGCTGGACCTTGGCGCCGGCGCCCTGCAG  
 ATCCCATTGCCATGCAGATGGCCTACCGCTTCAACGGCATGGCGTGAC  
 CCAGAACGTGCTGTACGAGAACAGAACAGATGCCAACCAAGTTAAC  
 AAGGCCATCTCCAGATCCAGGAGTCCCTGACCAACCTCCACCGCCCT  
 GGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCAGGCCCT  
 GAACACCCCTGGTGAAGCAGCTGTCCTCCAACCTCGGCCATCTCCG  
 TGCTGAACGACATCCTGTCCCGCTGGACAAGGTGGAGGCCAGGTGCA  
 GATCGACCGCCTGATCACCGCCGCTGCAGTCCCTGCAGACACTACGTG  
 ACCCAGCAGCTGATCCGCCGCCGAGATCCGCCCTCCGCCAACCTGG  
 CGGCCACCAAGATGTCCGAGTGCCTGGCCAGTCCAAGCG  
 CGTGGACTTCTGCCGCCAGGGCTACCCACCTGATGTCCTCCACAGGCC  
 GCCCCACACGGCGGGTGTCTGCACGTGACCTACGTGCCATCCCAGG  
 AGCGCAACTTCGCCACCGCCCCAGCCATCTGCCACGAGGGCAAGGCCTA  
 CTTCCACGCGAGGGCGTGTGTTCAACGGC

**SEQ ID NO: 20**

SARs Spike glycoprotein Fragment I protein sequence without the N-linked glycosylation sites (807 amino acids encoded by SEQ ID NO: 19):

AVDCSQNPLAELKCSVKSFEIDKGIFYQTSNFRVPSGDVVRFPNIANLCPFGEVFAATKFPSVYA  
 WERKKISNCVADYSVLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGV  
 IADNYKLPDDFMGCVLAWNTRNIDATSTGNYYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTP  
 PALNCYWPLNDYGFYTTGIGYQPYRVVLSFELLNAPATVCGPLSTDLIKNCVNFNGLTG  
 TGVLTSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSITPGTNAASEAVLYQ  
 DVACTDVSTAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSL  
 RSTSQKSVIVAYTMSLGADSSIAYSANTIAPITNFAISITTEVMPVSMAKTSVDCNMVICGDSTEANL  
 LLQYGSFCTQLNRALSGIAEQDRNTREVFAQVKQMYKPTLKYGFFGNAQILPDPLKPTKRSFI  
 EDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATA  
 GWTFGAGAAQALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTSALGKLQ  
 DVVNQNAQALNTLVQLSSNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQLSQLTYVTQQLIRAA  
 EIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFPQAAPHGVFLHVTYVPSQERNFATAPAI  
 CHEGKAYFPREGFVFNG

**SEQ ID NO: 21: SARs Spike glycoprotein Fragment II synthetic DNA sequence with N-linked glycosylation site mutations (744bps):**

GTGCTGTACAACCTCCGCCTTCTTCTCACCTCAAGTGTACGGCGTGTC  
 CGCCACCAAGCTGAACGACCTGTGCTTCTCAACGTGTACGCCGACTCCT  
 TCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGG  
 CGTGATCGCCGACTACAACATACAAGCTGCCAGACGACTTCATGGGCTGC  
 GTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACT  
 ACAACTACAAGTACCGTACCTGCGCACGGCAAGCTGCGCCATTCTGA  
 GCGCGACATCTCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACC  
 CCACCAAGCCCTGAACGTGCTACTGCCACTGAACGACTACGGCTTCTACAC  
 CACCAACGGCATCGGCTACCAAGCCATACCGCGTGGTGGTGTCTCCTTC  
 GAGCTGCTGAACGCCAGCCACCGTGTGCGGCCAAAGCTGTCCACCG  
 ACCTGATCAAGAACCAAGTGCCTGAACCTCAACTTCAACCGCCTGACCGGC  
 ACCGGCGTGTGACCCCATTCTCCAAGCGCTTCCAGCCATTCCAGCAGTT  
 CGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGGACCCAAAGACC  
 TCCGAGATCCTGGACATCTCCCCATGCTCCTCGCGGGGTGTCCGTGAT  
 CACCCAGGCACCAACGCCCTCCGAGGTGGCCGTGTACCAAGGAC  
 GTG

**SEQ ID NO: 22: SARs Spike glycoprotein Fragment II protein sequence without the N-linked glycosylation sites (248amino acids, encoded by SEQ ID 21):**

VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADNYKLPDDFMG  
 CVLAWNTRNIDATSTGNYYKYRYLRHGKLRPFERDISNVPFSPDGKPCPTPALNCYWPLNDY  
 GFYTTGIGYQPYRVVLSFELLNAPATVCGPLSTDLIKNCVNFNGLTG  
 TGVLTSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSITPGTNAASEAVLYQDV

**SEQ ID NO: 23: SARS Spike glycoprotein Fragment III synthetic DNA sequence with N-linked glycosylation site mutations (834 bps):**

GCCGAGCAGGACCGAACACCCCGCAGGTGTTGCCAGGTGAAGCAGA  
 TGTACAAGACCCCAACCTGAAGTACTTCGGCGGCTTCAACTCGCCCAG  
 ATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTCATCGAGGACCT  
 GCTGTTCAACAAGGTGACCCCTGGCGACGCCGGCTTCATGAAGCAGTAC  
 GGCGAGTGCCTGGCGACATCAACGCCCGACCTGATCTGCGCCCAGA  
 AGTTCAACGGCCTGACCGTGTGCCACCACTGCTGACCGACGACATGAT

CGCCGCCTACACCGCCGCCCTGGTGTCCGGCACCGCCACCGCCGGCTGG  
 ACCTTCGGCGCCGGCGCCGCCCTGCAGATCCCATTGCCATGCAGATGG  
 CCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAGAA  
 CCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCCAGATCCAG  
 GAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGG  
 TGAACCAGAACGCCAGGCCCTGAACACCCCTGGTGAAGCAGCTGTCTC  
 CAACTTCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCCTGG  
 ACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGCCGCC  
 GCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCCGCCGCCAG  
 ATCCCGCCTCCGCAACCTGGCCGCCACCAAGATGTCCGAGTGCCTGC  
 TGGGCCAGTCCAAGCGCTGGACTTCTGGCAAGGGTACCAACCTG

**SEQ ID NO: 24: SARs Spike glycoprotein Fragment III protein sequence without the N-linked glycosylation sites (278 amino acids, encoded by SEQ ID NO: 23):**

AEQDRNTREVFAQVKQMYKPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQ  
 YGECLGDIARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQ  
 MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQLQESLTTSALGKLQDVNQNAQALNTLVKQLS  
 SNFGAISSVLNDILSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG  
 QSKRVDFCGKGYHL

**SEQ ID NO: 25: SARs Spike glycoprotein Fragment IV synthetic DNA sequence with N-linked glycosylation site mutations (2034 bps):**

GTGCTGTACAACCTCCGCCCTTCTCCACCTTCAAGTGTACGGCGTGTCCGCCACCAAGCT  
 GAACGACCTGTGCTTCTCAACGTGTACGCCACTCTCGTGGTGAAGGGCGACGACGTG  
 CGCCAGATCGCCCCAGGCCAGACCGCGTGATGCCACTACAACACTACAAGCTGCCAGAC  
 GACTTCATGGCTGCGTGTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCA  
 ACTACAACACTACAAGTACCGTACCTCGCCACGGCAAGCTGCCACTTGAGCGCGACAT  
 CTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCAACCCACCAGCCCTGAACGTCTAC  
 TGGCCACTGAACGACTACGGCTTCTACACCAACCCGGCATGGCTACAGCCATACCGCG  
 TGGTGGTGTGCTGCTTCAGCTGTAACGCCAGCCACCGTGTGGGCCAAAGCTGTC  
 CACCGACCTGATCAAGAACCAAGTGCCTGAACCTCAACTTCAACGCCCTGACCGGCACCGGC  
 GTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCGGCCGACGTGTC  
 ACTTCACCGACTCCGTGCGCACCCAAAGACCTCCGAGATCTGGACATCTCCCCATGTC  
 CTCGGCGCGTGTCCGTGATCACCCAGGCACCAACGCCCTCCGAGGTGGCGTGCT  
 GTACCAAGGACGTGGCCTGACCGACGTGTCCACGCCATCCACGCCGACCGACTGACCCC  
 AGCCTGGCGCATCTACTCCACCGGCAACAAACGTGTTCCAGACCCAGGCCGCTGCCTGATC  
 GGCGCCGAGCACGTGGACACCTCTACGAGTGCACATCCCAATGGCGCCGGCATCTGC  
 GCCTCTACCAACCGTGTCCCTGCTGCCTCCACCTCCCAGAACGTCATCGTGGCTTACA  
 CCATGCCCCTGGCGCCACTCCTCATCGCTACTCCGCAACACCCATGCCATCCCAAC  
 CAACTTCGCCATCTCATCACCACCGAGGTGATGCCAGTGTCCATGGCCAAGACCTCCGT  
 GACTGAAACATGTACATCTGGCGACTCCACCGAGTGCACCAACCTGCTGCTGAGTACG  
 GCTCCTCTGCACCCAGCTGAACCGCGCCCTGTCCGGCATGCCCGAGCAGGACCGCA  
 ACACCCCGGAGGTGTTCGCCAGGTGAAGCAGATGTACAAGACCCCAACCTGAAGTACTT  
 CGGCGGCTTCAACTCGCCAGATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCC  
 ATCGAGGACCTGCTGTTAACAAAGGTGACCCCTGGCCGACGCCGGCTCATGAAGCAGTACG  
 GCGAGTGCCTGGCGACATCAACGCCCGGACCTGATCTGCCGCCAGAAGTCAACGGCC  
 TGACCGTGTGCCACCACTGCTGACCGACGACATGATGCCGCCATACCCGCCCTGGT  
 GTCCGGCACCGCCACCGCCGGCTGGACCTTCCGGCCGGCCGCGCCCTGCAGATCCCATT  
 CGCCATGCAAGATGGCCTACCGCTTCAACGGCATGGCGTGAACCCAGAACGTGCTGAG  
 AACCGAGAACGAGATGCCAACCAAGCTAACAGGCCATCTCCAGATCCAGGAGTCC  
 CCACCAACCTCCACCGCCCTGGGAAGCTGAGGCCAGAACGAGCTGAGGAGTCC  
 TGAACACCCCTGGTGAAGCAGCTGCTCTCCAACTTCCGGCCCATCTCCGTGCTGAACGA  
 CATCCTGTCCCCCTGGACAAGGTGGAGGCCAGGGTGCAGATCGACCGCCTGATACCG  
 CCGCCTGCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGGCCGCCAGATCC  
 CGCCTCCGCCAACCTGGCCGCCACCAAGATGTCCGAGTGCCTGCTGGCCAGTCCAAGCG  
 CGTGGACTTCTGGCAAGGGTACCAACCTG

SEQ ID NO: 26: SARs Spike glycoprotein Fragment IV protein sequence without the N-linked glycosylation sites (678 amino acids, encoded by SEQ ID NO: 25):

VLYNSAFFSTFKCYGVSATKLNDLCSNVYADSFVVKGDDVRQIAPGQTGVIADNYKLPDDFMG  
CVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYG  
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTSSKRFQPF  
QQFGRDVSDFTDSVRDPKTSEILDISPCSFGGVSVTPGTNAASEEVAVLYQDVACTDVSTAIHADQ  
LTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSL  
GADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRA  
LSGIAAEQDRNTRREVFAQVKQMYKTPTLKYYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTLADAG  
FMKQYGECLGDINARDLICAQKFNGLTVLPLLTDMMIAAYTAALVSGTATAGWTFGAGAALQIPF  
AMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLV  
KQLSSNFGAISSVLDILSRLDKVEAEVQIDRLITGRLQLSQLTYVTQQLIRAAEIRASANLAATKMSE  
CVLGQSkrVDFCGKGYHL